

SEQ ID NO: 14

09JM59

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ID   Q9JM59                PRELIMINARY;          PRT;       270 AA.
AC   Q9JM59;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   A-TYPE POTASSIUM CHANNEL MODULATORY PROTEIN 2B.
GN   RKCHIP2B.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Ohya S., Imaizumi Y.;
RT   "A-type potassium channel modulatory protein 2b.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC   -- SIMILARITY: TO EF-HAND FAMILY.
DR   EMBL; AB040032; BAA92744.1; -.
DR   InterPro; IPR001125; -.
DR   InterPro; IPR002048; -.
DR   Pfam; PF00036; efhand; 3.
DR   PRINTS; PR00450; RECOVERIN.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_3.
DR   SMART; SM00054; EFh; 1.
KW   Calcium-binding; Ionic channel.
SO   SEQUENCE 270 AA; 30933 MW; 3F70A64A159679DD CRC64;

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Query Match 98.9%; Score 1412; DB 11; Length 270;
Best Local Similarity 98.9%; Pred. No. 8.6e-109;
Matches 267; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MRGQGRKESLSDSRDLGSDYDLTGHPGPTKKALKQRFLKLLPCCGPQALPSVSETLAA	60
Db	1	MRGQGRKESLSDSRDLGSDYDLTGHPGPTKKALKQRFLKLLPCCGPQVLPSVSETLAA	60
Qy	61	PASLRPHRPRLLDPDSVDDEFELSTVCHRPEGLEQLQEQTKFTRKELQVLYRGFKNECP	120
		:	
Db	61	PASLRPHRPRPLDPDSVEDEFELSTVCHRPEGLEQLQEQTKFTRKELQVLYRGFKNECP	120
Qy	121	GIVNEENFKQIYSQFFPQDGSSTYATFLFNAFDTNHDSVSVFEDFVAGLSVILRGTVDDR	180
Db	121	GIVNEENFKQIYSQFFPQDGSSTYATFLFNAFDTNHDSVSVFEDFVAGLSVILRGTVDDR	180
Qy	181	LNWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDR	240
Db	181	LNWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDR	240
Qy	241	DGVVTIEEFIESCQKDENIMRSMQLFDNVI	270
Db	241	DGVVTIEEFIESCOKDENIMRSMQLFDNVI	270

Q9NS61

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ID   Q9NS61          PRELIMINARY;          PRT;   270 AA.
AC   Q9NS61;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   POTASSIUM CHANNEL-INTERACTING PROTEIN 2B.
GN   KCHIP2B.

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OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=UMBILICAL ENDOTHELIAL CELL;
 RA Ohya S., Imaizumi Y.;
 RT "human potassium channel interacting protein 2b.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL; AB044584; BAA96740.1; -.
 DR InterPro; IPR001125; -.
 DR InterPro; IPR002048; -.
 DR Pfam; PF00036; efhand; 3.
 DR PRINTS; PR00450; RECOVERIN.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
 DR SMART; SM00054; EFh; 1.
 KW Calcium-binding.
 SQ SEQUENCE 270 AA; 30959 MW; 22DBD64A15966D98 CRC64;

Query Match 98.6%; Score 1407; DB 4; Length 270;
 Best Local Similarity 98.5%; Pred. No. 2.2e-108;
 Matches 266; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 MRGQGRKESLSDSRDLGSDYDQLTGHPGPTKKALKQRFLKLLPCCGPQALPSVSETLAA 60
        |||
Db      1 MRGQGRKESLSDSRDLGSDYDQLTGHPGPTKKALKQRFLKLLPCCGPQVLPVSVSETLAA 60

Qy     61 PASLRPHRPRLLDPDSVDEFELSTVCHRPEGLEQLQEQTKEFTRKELQVLYRGFKNECPS 120
        |||
Db     61 PASLRPHRPRPLDPDSVEDEFELSTVCHRPEGLEQLQEQTKEFTRKELQVLYRGFKNECPS 120

Qy    121 GIVNEENFKQIYSQFFPQGDSSTYATFLFNAFDTNHDGSVSFEDFVAGLSVILRGTVDDR 180
        |||
Db    121 GIVNEENFKQIYSQFFPQGDSSTYATFLFNAFDTNHDGSVSFEDFVAGLSVILRGTVDDR 180

Qy    181 LNWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRKN 240
        |||
Db    181 LNWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEPPREHVESFFQKMDRKN 240

Qy    241 DGVVTIEEFIESCQKDENIMRSMQLFDNVI 270
        |||
Db    241 DGVVTIEEFIESCQKDENIMRSMQLFDNVI 270
  
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RESULT 3

Q9JJ69

ID Q9JJ69 PRELIMINARY; PRT; 270 AA.
 AC Q9JJ69;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE POTASSIUM CHANNEL-INTERACTING PROTEIN 2A.
 GN KCHIP2A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Ohya S., Imaizumi Y.;
 RT "mouse potassium channel interacting protein 2a (KCHIP2a).";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL; AB044570; BAA96738.1; -.
 DR InterPro; IPR001125; -.
 DR InterPro; IPR002048; -.
 DR Pfam; PF00036; efhand; 3.

DR PRINTS; PR00450; RECOVERIN.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
DR SMART; SM00054; EFh; 1.
KW Calcium-binding.
SQ SEQUENCE 270 AA; 30906 MW; 917E564A159679C1 CRC64;

Query Match 98.6%; Score 1407; DB 11; Length 270;
Best Local Similarity 98.5%; Pred. No. 2.2e-108;
Matches 266; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 MRGQGRKESLSDSRDLGSDYDLTGHPGPTKKALKQRFLKLLPCCGPQALPSVSETLAA 60
          |||
Db      1 MRGQGRKESLSDSRDLGSDYDLTGHPGPTKKALKQRFLKLLPCCGPQVLPVSETLAA 60

Qy     61 PASLRPHRPRLLDPDSVDEFEFELSTVCHRPEGLEQLQEQTKEFTRKELQVLYRGFKNECP 120
          |||
Db     61 PASLRPHRPRPLDPDSVEDEFELSTVCHRPEGLEQLQEQTKEFTRKELQVLYRGFKNECP 120

Qy    121 GIVNEENFKQIYSQFFPQGDSTYATFLFNAFDTNHDGVSFEDFVAGLSVILRGTVDDR 180
          |||
Db    121 GIVNEENFKQIYSQFFPQGDSTYATFLFNAFDTNHDGVSFEDFVAGLSVILRGTVDDR 180

Qy    181 LNWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRKN 240
          |||
Db    181 LNWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRSK 240

Qy    241 DGVVTIEEFIESCQKDENIMRSMQLFDNVI 270
          |||
Db    241 DGVVTIEEFIESCQKDENIMRSMQLFDNVI 270
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RESULT 4

Q9JI23

ID Q9JI23 PRELIMINARY; PRT; 270 AA.
AC Q9JI23;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE POTASSIUM CHANNEL AUXILIARY SUBUNIT KCHIP2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Takimoto K.;
RT "Potassium channel auxiliary subunit KCHIP2 splicing variant."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO EF-HAND FAMILY.
DR EMBL; AF269283; AAF81755.1; -.
DR InterPro; IPR001125; -.
DR InterPro; IPR002048; -.
DR Pfam; PF00036; efhand; 3.
DR PRINTS; PR00450; RECOVERIN.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
DR SMART; SM00054; EFh; 1.
KW Calcium-binding.
SQ SEQUENCE 270 AA; 30932 MW; C797DEC90FDC3B92 CRC64;

Query Match 97.4%; Score 1390; DB 11; Length 270;
Best Local Similarity 96.7%; Pred. No. 5.6e-107;
Matches 261; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 MRGQGRKESLSDSRDLGSDYDLTGHPGPTKKALKQRFLKLLPCCGPQALPSVSETLAA 60
          |||
Db      1 MRGQGRKESLSERDLGSDYDLTGHPGPTKKALKQRFLKLLPCCGPQALPSVSETLAA 60

Qy     61 PASLRPHRPRLLDPDSVDEFEFELSTVCHRPEGLEQLQEQTKEFTRKELQVLYRGFKNECP 120
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Db      61 PASLRPHRPRPLDPDSVEDEFELSTVCHRPEGLEQLQEQTKEFTRRELQVLYRGFKNECPS 120
Qy      121 GIVNEENFKQIYSQFFPQGDSSYATFLFNAFDTNHDGSVSFEDFVAGLSVILRGTVDDR 180
Db      121 GIVNEENFKQIYSQFFPQGDSSNYATFLFNAFDTNHDGSVSFEDFVAGLSVILRGTIDDR 180
Qy      181 LNWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRKN 240
Db      181 LSWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVESFFQKMDRKN 240
Qy      241 DGVVTIEEFIESCQKDENIMRSMQLFDNVI 270
Db      241 DGVVTIEEFIESCQQDENIMRSMQLFDNVI 270

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SEQ ID NO: 26

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RESULT 1
US-09-048-889-3
; Sequence 3, Application US/09048889
; Patent No. 6117989
; GENERAL INFORMATION:
;   APPLICANT: Bandman, Olga
;   APPLICANT: Hillman, Jennifer L.
;   APPLICANT: Corley, Neil C.
;   APPLICANT: Guegler, Karl J.
;   APPLICANT: Lal, Preeti
;   APPLICANT: Patterson, Chandra
;   TITLE OF INVENTION: HUMAN CALCIUM-BINDING PROTEINS
;   NUMBER OF SEQUENCES: 11
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Incyte Pharmaceuticals, Inc.
;     STREET: 3174 Porter Drive
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/048,889
;     FILING DATE: Herewith
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Cerrone, Michael C
;     REGISTRATION NUMBER: 39,132
;     REFERENCE/DOCKET NUMBER: PF-0493 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 650-855-0555
;     TELEFAX: 650-845-4166
;     TELEX:
;   INFORMATION FOR SEQ ID NO: 3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 188 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     IMMEDIATE SOURCE:
;       LIBRARY: BRAINON01

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; CLONE: 2287407
US-09-048-889-3

Query Match 71.7%; Score 830; DB 3; Length 188;
Best Local Similarity 79.3%; Pred. No. 3.1e-82;
Matches 149; Conservative 26; Mismatches 13; Indels 0; Gaps 0;

Qy	33	LSTVCHRPEGLEQLQEQTKFTRKELQVLYRGFKNECPSGIVNEENFKQIYSQFFPQGDSS	92
Db	1	MATVRRHPEALELLEAQSKEFTKKEFQILYRGFKNECPSGVNEETFEKIEYSQFFPQGDST	60
Qy	93	TYATFLFNAFDTNHDGVSVSFEDFVAGLSVILRGTVDDRLNWFNLYDLNKDGCITKEEML	152
Db	61	TYAHFLFNAFDTDHNGAVSFEDFIKGLSILLRGTVQEKLNWAFNLYDINKDGYITKEEML	120
Qy	153	DIMKSIYDMMGKYTYPALREEAPREHVENFFQKMDRNDKGVVITIEEFIESCQKDENIMRS	212
Db	121	DIMKAIYDMMGKCTYPVLKEDAPRQHVETFFQKMDKNKDGVVITIDEFIESCQEDENIMRS	180
Qy	213	MQLFDNVI	220
Db	181	MOLFENVI	188

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RESULT 1
Q9JM60
ID Q9JM60 PRELIMINARY; PRT; 220 AA.
AC Q9JM60;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE A-TYPE POTASSIUM CHANNEL MODULATORY PROTEIN 2A.
GN RKCHIP2A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Ohya S., Imaizumi Y.;
RT "A-type potassium channel modulatory protein 2a.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBDJ databases.
CC -!- SIMILARITY: TO EF-HAND FAMILY.
DR EMBL; AB040031; BAA92743.1; -.
DR InterPro; IPR001125; -.
DR InterPro; IPR002048; -.
DR Pfam; PF00036; efhand; 3.
DR PRINTS; PR00450; RECOVERIN.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
DR SMART; SM00054; EFh; 1.
KW Calcium-binding; Ionic channel.
SO SEQUENCE 220 AA; 25576 MW; A7093C9456A2838E CRC64;

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Query Match 99.6%; Score 1152; DB 11; Length 220;
Best Local Similarity 99.5%; Pred. No. 3.9e-84;
Matches 219; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

[illegible]

Qy 181 NFFQKMDRNKDGVVTTIEEFIESCQKDENIMRSMQLFDNVI 220
 :|||||
 Db 181 SFFQKMDRNKDGVVTTIEEFIESCQKDENIMRSMQLFDNVI 220

RESULT 2

Q9HD11

ID Q9HD11 PRELIMINARY; PRT; 220 AA.
 AC Q9HD11;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE CARDIAC VOLTAGE GATED POTASSIUM CHANNEL MODULATORY SUBUNIT, SHORT FORM
 DE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CARDIAC;
 RA Juang G.J., Tomaselli G.F.;
 RT "Modulatory elements of voltage gated potassium channels.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF295076; AAG02120.1; -.
 KW Ionic channel.
 FT NON_TER 220 220
 SQ SEQUENCE 220 AA; 25562 MW; 52FD8C601356338F CRC64;

Query Match 99.3%; Score 1149; DB 4; Length 220;
 Best Local Similarity 99.1%; Pred. No. 6.7e-84;
 Matches 218; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGQGRKESLSDSRDLGSDYDQLTDSVEDEFELSTVCHRPEGLEQLQEQTKFTRKELQVL 60
 |||||
 Db 1 MRGQGRKESLSDSRDLGSDYDQLTDSVDEDEFELSTVCHRPEGLEQLQEQTKFTRKELQVL 60
 Qy 61 YRGFKNECPGIVNEENFKQIYSQFFPQGSSTYATFLFNAFDTNHDGVSFEDFVAGLS 120
 |||||
 Db 61 YRGFKNECPGIVNEENFKQIYSQFFPQGSSTYATFLFNAFDTNHDGVSFEDFVAGLS 120
 Qy 121 VILRGTVDDRLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVE 180
 |||||
 Db 121 VILRGTVDDRLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVE 180
 Qy 181 NFFQKMDRNKDGVVTTIEEFIESCQKDENIMRSMQLFDNVI 220
 :|||||
 Db 181 SFFQKMDRNKDGVVTTIEEFIESCQKDENIMRSMQLFDNVI 220

RESULT 3

Q9JJ68

ID Q9JJ68 PRELIMINARY; PRT; 220 AA.
 AC Q9JJ68;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE POTASSIUM CHANNEL-INTERACTING PROTEIN 2B.
 GN KCHIP2B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Ohya S., Imaizumi Y.;
 RT "mouse potassium channel interacting protein 2b (mKChIP2b).";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL; AB044571; BAA96739.1; -.
 DR InterPro; IPR001125; -.
 DR InterPro; IPR002048; -.
 DR Pfam; PF00036; efhand; 3.
 DR PRINTS; PR00450; RECOVERIN.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
 DR SMART; SM00054; EFh; 1.
 KW Calcium-binding.
 SQ SEQUENCE 220 AA; 25549 MW; 0907CC9456A28392 CRC64;

Query Match 99.1%; Score 1147; DB 11; Length 220;
 Best Local Similarity 99.1%; Pred. No. 9.7e-84;
 Matches 218; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGQGRKESLSDSRDLGSDYDQLTDSVEDEFELSTVCHRPEGLEQLQEQTkFTRKELQVL 60
 |||
 Db 1 MRGQGRKESLSDSRDLGSDYDQLTDSVEDEFELSTVCHRPEGLEQLQEQTkFTRKELQVL 60
 Qy 61 YRGFKNECPGSGIVNEENFKQIYSQFFPQGDSSYATFLFNAFDTNHDGVSFEDFVAGLS 120
 |||
 Db 61 YRGFKNECPGSGIVNEENFKQIYSQFFPQGDSSYATFLFNAFDTNHDGVSFEDFVAGLS 120
 Qy 121 VILRGTVDDRNLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVE 180
 |||
 Db 121 VILRGTVDDRNLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVE 180
 Qy 181 NFFQKMDRKNKDGVTIEEFIESCQKDENIMRSMQLFDNVI 220
 :|||
 Db 181 SFFQKMDRSKDGVTIEEFIESCQKDENIMRSMQLFDNVI 220

RESULT 4

Q9NS60

ID Q9NS60 PRELIMINARY; PRT; 220 AA.
 AC Q9NS60;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE POTASSIUM CHANNEL-INTERACTING PROTEIN 2C.
 GN KCHIP2C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=UMBILICAL ENDOTHELIAL CELL;
 RA Ohya S., Imaizumi Y.;
 RT "human potassium channel interacting protein 2b."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL; AB044585; BAA96741.1; -.
 DR InterPro; IPR001125; -.
 DR InterPro; IPR002048; -.
 DR Pfam; PF00036; efhand; 3.
 DR PRINTS; PR00450; RECOVERIN.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
 DR SMART; SM00054; EFh; 1.
 KW Calcium-binding.
 SQ SEQUENCE 220 AA; 25586 MW; 57985A40F4CC3B1F CRC64;

Query Match 98.4%; Score 1138; DB 4; Length 220;
 Best Local Similarity 98.6%; Pred. No. 5e-83;
 Matches 217; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRGQGRKESLSDSRDLGSDYDQLTDSVEDEFELSTVCHRPEGLEQLQEQTkFTRKELQVL 60
 |||
 Db 1 MRGQGRKESLSDSRDLGSDYDQLTVSVEDEFELSTVCHRPEGLEQLQEQTkFTRKELQVL 60

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Qy      61 YRGFKNECPGIVNEENFKQIYSQFFPQGDSSTYATFLFNAFDTNHDGVSFEDFVAGLS 120
        |||
Db      61 YRGFKNECPGIVNEENFKQIYSQFFPQGDSSTYATFLFNAFDTNHDGVSFEDFVAGLS 120

Qy     121 VILRGTVDDRLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVE 180
        |||
Db     121 VILRGTVDDRLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEPPREHVE 180

Qy     181 NFFQKMDRNDKGVVTIEEFIESCQKDENIMRSMQLFDNVI 220
        :|||
Db     181 SFFQKMDRNDKGVVTIEEFIESCQKDENIMRSMQLFDNVI 220

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RESULT 5

Q9HD10

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ID  Q9HD10      PRELIMINARY;      PRT;    227 AA.
AC  Q9HD10;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT  01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE  CARDIAC VOLTAGE GATED POTASSIUM CHANNEL MODULATORY SUBUNIT.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=CARDIAC;
RA  Juang G.J., Wu R.C., Tomaselli G.F.;
RT  "Modulatory elements of voltage gated potassium channels.";
RL  Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; AF295530; AAG02121.1; -.
KW  Ionic channel.
SQ  SEQUENCE 227 AA; 26263 MW; 7F1D2B8E7F85D8B9 CRC64;

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```

Query Match          98.1%; Score 1135.5; DB 4; Length 227;
Best Local Similarity 96.0%; Pred. No. 8.2e-83;
Matches 218; Conservative 2; Mismatches 0; Indels 7; Gaps 1;

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Qy      1 MRGQGRKESLSDSRDLGSDYQLTDSVEDEFELSTVCHRPEGLEQLQEQTKEFTRKELQVL 60
        |||
Db      1 MRGQGRKESLSDSRDLGSDYQLTDSVEDEFELSTVCHRPEGLEQLQEQTKEFTRKELQVL 60

Qy     61 YRGFKN-----ECPGIVNEENFKQIYSQFFPQGDSSTYATFLFNAFDTNHDGVSFE 113
        |||
Db     61 YRGFKNPGALSFECPGIVNEENFKQIYSQFFPQGDSSTYATFLFNAFDTNHDGVSFE 120

Qy    114 DFVAGLSVILRGTVDDRLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREE 173
        |||
Db    121 DFVAGLSVILRGTVDDRLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREE 180

Qy    174 APREHVENFFQKMDRNDKGVVTIEEFIESCQKDENIMRSMQLFDNVI 220
        |||
Db    181 APREHVESFFQKMDRNDKGVVTIEEFIESCQKDENIMRSMQLFDNVI 227

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RESULT 6

Q9JI21

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ID  Q9JI21      PRELIMINARY;      PRT;    220 AA.
AC  Q9JI21;
DT  01-OCT-2000 (TrEMBLrel. 15, Created)
DT  01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT  01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE  POTASSIUM CHANNEL AUXILIARY SUBUNIT KCHIP2C.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]

```


RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Takimoto K.;
 RT "Potassium channel auxiliary subunit KCHIP2 splicing variant.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL; AF269285; AAF81757.1; -.
 DR InterPro; IPR001125; -.
 DR InterPro; IPR002048; -.
 DR Pfam; PF00036; efhand; 3.
 DR PRINTS; PR00450; RECOVERIN.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
 DR SMART; SM00054; EFh; 1.
 KW Calcium-binding.
 SQ SEQUENCE 220 AA; 25618 MW; 519D144AB55A9BBC CRC64;

Query Match 97.7%; Score 1130; DB 11; Length 220;
 Best Local Similarity 96.8%; Pred. No. 2.2e-82;
 Matches 213; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MRGQGRKESLSDSRDLGSDYQLTDSVEDEFELSTVCHRPEGLEQLQEQTkFTRKELQVL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MRGQGRKESLSERDLGSDYQLTDSVEDEFELSTVCHRPEGLEQLQEQTkFTRRELQVL 60

Qy     61 YRGFKNECPGIVNEENFKQIYSQFFPQGDSSYATFLFNAFDTNHDGVSVSFEDFVAGLS 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     61 YRGFKNECPGIVNEENFKQIYSQFFPQGDSSYATFLFNAFDTNHDGVSVSFEDFVAGLS 120

Qy    121 VILRGTVDDRNLNWFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVE 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    121 VILRGTIIDRLSWAFNLYDLNKDGCITKEEMLDIMKSIYDMMGKYTPALREEAPREHVE 180

Qy    181 NFFQKMDRNRKDGVVTTIEEFIESCQKDENIMRSMQLFDNVI 220
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    181 SFFQKMDRNRKDGVVTTIEEFIESCQKDENIMRSMQLFDNVI 220
  
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SEQ ID NO: 18

RESULT 14
 US-08-764-563-3
 ; Sequence 3, Application US/08764563
 ; Patent No. 6093565
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/764,563
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-328-322-17

Query Match 13.4%; Score 191; DB 1; Length 174;
Best Local Similarity 29.5%; Pred. No. 5.5e-13;
Matches 52; Conservative 42; Mismatches 66; Indels 16; Gaps 6;

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Qy 93 LEQLQEQTkFTRRELQVLYRGFK--NECPsGIVNEENFKQIYSQFFPQGDSSNYATFLFN 150
   :: || || || || :: || : | : || :: | | | | : | :
Db 9 VDGLLEDtNFDRDEIERLRKRfMKLDRDSSGSIDKNEFMSI-----PGVSSNPLAGRIME 63

Qy 151 AFDtNHdGSVSfEDfVAGLSvIL-RGTIDDRLNWAFNLYDLNKdGCITKEEMLDIMKSIY 209
   || :: | | | :: | : || : || : || : || : || | : | : :: |
Db 64 VFDADNSGDVDFQEFITGLSIFSGRGSKDEKLRFaFKIYDIDKdGFISNGELFIVLKI-- 121

Qy 210 DMMGKYtYPALREEAPREHVESFFQKMDRNKdGVVTIEEFIESCQqDENIMRSMQL 265
   | : | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 122 -MVGS----NLDDEQLQqIVDRtIVENDSDGDGRLSFEeFKNAIETTE-VAKSLTL 171
```